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95. The isolated nucleic acid of claim 68 comprising a polynucleotide comprising at least 50 contiguous bases of SEQ ID NO: 1 or a polynucleotide fully complementary thereof.

96. The isolated nucleic acid of claim 68 comprising a polynucleotide comprising at least 100 contiguous bases of SEQ ID NO: 1 or a polynucleotide fully complementary thereof.--

REMARKS

Reconsideration of the present application is respectfully requested. Claims 4-12, 15-27, 30-40 and 43-94 are in the application. Claims 63-67, 73-77 and 83-92 are allowed. Claims 16-27, 30-40, 43-61 and 93-94 are cancelled without prejudice. New claims 95-96 are added. Support for the new claims is found on page 5, line 24 to page 6, line 4 and page 12, lines 16-22 as well as other portions of the present application.

Claims 4-12, 15, 33, 48-49, 62 and 78-82 are rejected under 35 USC 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 62 and 78 have been amended to recite high stringency hybridization conditions. Support for the amendment is found on page 15, lines 9-10. The term "selectively" has been removed from the claims. It is submitted that the amendment does not narrow the claims, as "high stringency conditions" was originally recited in the claims and defined in the specification.

Claim 9 has been amended to depend from claim 62.

Claims 33 and 48-49 have been cancelled without prejudice.

Claims 4-12, 15, 33, 62 and 68-72 are rejected under 35 USC 112, first paragraph.

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The Examiner states that the specification is enabling for an isolated polynucleotide of SEQ ID NO:1, a polynucleotide having at least 80% sequence identity thereto and a polynucleotide that is fully complementary to the polynucleotides, capable of modulating LEC1 protein and transgenic plants, plant cells and seeds.

The Examiner further states that enablement is not provided for an isolated polynucleotide comprising any 20 contiguous bases of SEQ ID NO:1 that is capable of modulating LEC1 protein.

The statement is traversed. However, claim 62 has been amended to remove reference to "an isolated polynucleotide comprising any 20 contiguous bases" in order to expedite prosecution of that claim. Claim 68 has been amended to remove the required function. The Examiner's attention is directed to page 5, line 24 to page 6, line 4 and page 12, lines 16-22 for a discussion of the function of fragments and their use as primers, probes and antisense fragments. The particular fragment used is not critical to the invention. Those skilled in the art can readily select an appropriate fragment from the sequences and the information provided in the present application.

Claims 4-12, 15, 62, 78-82 and new claims are rejected under 35 USC 102(e) as being anticipated by Harada et al US 6,235,975.

Claims 62 and 78 have been amended to recite specific hybridization conditions. The term "selectively" has been removed from the claims. It is submitted that the amendment does not narrow the claims, as "high stringency conditions" was originally recited in the claims and defined in the specification.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned **"Version with markings to show changes made."**

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In view of the above amendments and comments, withdrawal of all of the rejections and allowance of the remaining claims is respectfully requested.

Respectfully submitted, –

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Claims:

Claims 16-27, 30-40, 43-61 and 93-94 have been cancelled without prejudice.

Claims 9, 62, 68, and 78 have been amended as follows:

9.   (Twice Amended) A transgenic plant comprising an isolated nucleic acid of claim [1] 62.

62.   (Amended) An isolated nucleic acid capable of modulating the level of LEC1 protein, the isolated nucleic acid comprising a member selected from the group consisting of:

     (a)   a polynucleotide which encodes a polypeptide of SEQ ID NO: 2;

     [(b)   a polynucleotide comprising at least 20 contiguous bases of SEQ ID NO: 1;]

     [(c)](b) a polynucleotide having at least 80% sequence identity to the entire coding sequence of SEQ ID NO: 1, wherein the % sequence identity is determined by GAP analysis using Gap Weight of 50 and Length Weight of 3;

     [(d)](c) a polynucleotide which [selectively] hybridizes under high stringency conditions to the polynucleotide of SEQ ID NO: 1, wherein high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60°C;

     [(e)](d) a polynucleotide having the sequence set forth in SEQ ID NO: 1; and

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[(f)](e) a polynucleotide fully complementary to a polynucleotide of (b)
through [(e)](d).

68.   An isolated nucleic acid [capable of modulating the level of LEC1 protein, the
isolated nucleic acid] comprising a polynucleotide comprising at least 20
contiguous bases of SEQ ID NO: 1 or a polynucleotide fully complementary
thereof.

78.   An isolated nucleic acid capable of modulating the level of LEC1 protein, the
isolated nucleic acid comprising a polynucleotide which [selectively]
hybridizes under high stringency conditions to the polynucleotide of SEQ ID
NO: 1 or a polynucleotide fully complementary thereof, wherein high
stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1%
SDS at 37°C, and a wash in 0.1X SSC at 60°C.

New claims 95 and 96 have been added as follows:

95.   The isolated nucleic acid of claim 68 comprising a polynucleotide comprising
at least 50 contiguous bases of SEQ ID NO: 1 or a polynucleotide fully
complementary thereof.

96.   The isolated nucleic acid of claim 68 comprising a polynucleotide comprising
at least 100 contiguous bases of SEQ ID NO: 1 or a polynucleotide fully
complementary thereof.

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